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JUN 2004

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Ihr Zeichen/Your ref.:

Unser Zeichen/Our file:
P23795

Bearbeiter:
sd/ws

Datum/Date:
18.03.2004

International Patent Application PCT/EP03/14542
"Novel Chimeric Plasminogen Activators and Their Pharmaceutical Use"
Appl.: Prof. Dr. Werner Seeger

In reply to the Communication dated February 20, 2004,

an amended sequence listing is filed herewith in written form as well as in computer-readable form (ASCII format; file name: 23795_seq.txt) saved on the enclosed diskette.

The amended sequence listing does not go beyond the disclosure in the application as filed. It now includes the pure amino acid sequences of SEQ ID NOs 1 to 13, which are referred to as SEQ ID NOs 14 to 26, respectively.

Encl.
Sequence listing, paper copy
Diskette

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Patentanwalt

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AP20 Rec'd PCT/PTO 19 JUN 2006

SEQUENCE LISTING

<110> Prof. Dr. Werner Seeger
 <120> Novel chimeric plasminogen activators and their pharmaceutical use
 <160> 26

<210> 1
 <211> 1143
 <212> DNA
 <213> Homo sapiens

<220>
 <221> CDS
 <222> (1) ... (1143)
 <223> Coding sequence of the surfactant protein B precursor

<400> 1

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| Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr | |
| 1 5 10 15 | |
| ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt | 96 |
| Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys | |
| 20 25 30 | |
| gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag | 144 |
| Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln | |
| 35 40 45 | |
| tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga | 192 |
| Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly | |
| 50 55 60 | |
| gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac | 240 |
| Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn | |
| 65 70 75 80 | |
| aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg | 288 |
| Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu | |
| 85 90 95 | |
| gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc | 336 |
| Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys | |
| 100 105 110 | |
| aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag | 384 |
| Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln | |
| 115 120 125 | |
| aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa | 432 |
| Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys | |
| 130 135 140 | |
| tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg | 480 |
| Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu | |
| 145 150 155 160 | |
| ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc | 528 |

| | |
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| Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu | |
| 165 170 175 | |
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| Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His | |
| 180 185 190 | |
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| Thr Gln Asp Leu Ser Glu Gln Phe Pro Ile Pro Leu Pro Tyr Cys | |
| 195 200 205 | |
| tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag | 672 |
| Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys | |
| 210 215 220 | |
| ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg | 720 |
| Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu | |
| 225 230 235 240 | |
| gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc | 768 |
| Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile | |
| 245 250 255 | |
| ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc | 816 |
| Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg | |
| 260 265 270 | |
| ctc gtc ctc cgg tgc tcc atg gat gac agc gct ggc cca agg tgc ccg | 864 |
| Leu Val Leu Arg Cys Ser Met Asp Asp Ser Ala Gly Pro Arg Ser Pro | |
| 275 280 285 | |
| aca gga gaa tgg ctg ccg cga gac tct gag tgc cac ctc tgc atg tcc | 912 |
| Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser | |
| 290 295 300 | |
| gtg acc acc cag gcc ggg aac agc agc gag cag gcc ata cca cag gca | 960 |
| Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala | |
| 305 310 315 320 | |
| atg ctc cag gcc tgt gtt ggc tcc tgg ctg gac agg gaa aag tgc aag | 1008 |
| Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys | |
| 325 330 335 | |
| caa ttt gtg gag cag cac acg ccc cag ctg ctg acc ctg gtg ccc agg | 1056 |
| Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg | |
| 340 345 350 | |
| ggc tgg gat gcc cac acc acc tgc cag gcc ctc ggg gtg tgt ggg acc | 1104 |
| Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr | |
| 355 360 365 | |
| atg tcc agc cct ctc cag tgt atc cac agc ccc gac ctt | 1143 |
| Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu | |
| 370 375 380 | |

<210> 2
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 <212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (837)

<223> Coding sequence of the surfactant protein B precursor lacking the C-terminal propeptide

<400> 2

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| atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg | 48 |
| Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr | |
| 1 5 10 15 | |
| ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt | 96 |
| Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys | |
| 20 25 30 | |
| gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag | 144 |
| Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln | |
| 35 40 45 | |
| tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga | 192 |
| Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly | |
| 50 55 60 | |
| gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac | 240 |
| Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn | |
| 65 70 75 80 | |
| aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg | 288 |
| Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu | |
| 85 90 95 | |
| gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc | 336 |
| Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys | |
| 100 105 110 | |
| aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag | 384 |
| Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln | |
| 115 120 125 | |
| aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa | 432 |
| Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys | |
| 130 135 140 | |
| tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg | 480 |
| Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu | |
| 145 150 155 160 | |
| ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc | 528 |
| Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu | |
| 165 170 175 | |
| gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac | 576 |
| Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His | |
| 180 185 190 | |
| aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc | 624 |

Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys
195 200 205

tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag 672
Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys
210 215 220

ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg 720
Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu
225 230 235 240

gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc 768
Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile
245 250 255

ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc 816
Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg
260 265 270

ctc gtc ctc cgg tgc tcc atg 837
Leu Val Leu Arg Cys Ser Met
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<210> 3
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<212> DNA
<213> Homo sapiens

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<221> CDS
<222> (1) ... (237)
<223> Coding sequence of the mature surfactant protein B

<400> 3

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Phe Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys
1 5 10 15

cgg atc caa gcc atg att ccc aag ggt gcg cta gct gtg gca gtg gcc 96
Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala
20 25 30

cag gtg tgc cgc gtg gta cct ctg gtg gcg ggc ggc atc tgc cag tgc 144
Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys
35 40 45

ctg gct gag cgc tac tcc gtc atc ctg ctc gac acg ctg ctg ggc cgc 192
Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg
50 55 60

atg ctg ccc cag ctg gtc tgc cgc ctc gtc ctc cgg tgc tcc atg 237
Met Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met
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<210> 4
<211> 1293

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1293)

<223> Coding sequence of the single-chain urokinase-plasminogen activator

<400> 4

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| atg aga gcc ctg ctg gcg cgc ctg ctt ctc tgc gtc ctg gtc gtg agc | 48 |
| Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser | |
| 1 5 10 15 | |
| gac tcc aaa ggc agc aat gaa ctt cat caa gtt cca tcg aac tgt gac | 96 |
| Asp Ser Lys Gly Ser Asn Glu Leu His Gln Val Pro Ser Asn Cys Asp | |
| 20 25 30 | |
| tgt cta aat gga gga aca tgt gtg tcc aac aag tac ttc tcc aac att | 144 |
| Cys Leu Asn Gly Gly Thr Cys Val Ser Asn Lys Tyr Phe Ser Asn Ile | |
| 35 40 45 | |
| cac tgg tgc aac tgc cca aag aaa ttc gga ggg cag cac tgt gaa ata | 192 |
| His Trp Cys Asn Cys Pro Lys Lys Phe Gly Gly Gln His Cys Glu Ile | |
| 50 55 60 | |
| gat aag tca aaa acc tgc tat gag ggg aat ggt cac ttt tac cga gga | 240 |
| Asp Lys Ser Lys Thr Cys Tyr Glu Gly Asn Gly His Phe Tyr Arg Gly | |
| 65 70 75 80 | |
| aag gcc agc act gac acc atg ggc cgg ccc tgc ctg ccc tgg aac tct | 288 |
| Lys Ala Ser Thr Asp Thr Met Gly Arg Pro Cys Leu Pro Trp Asn Ser | |
| 85 90 95 | |
| gcc act gtc ctt cag caa acg tac cat gcc cac aga tct gat gct ctt | 336 |
| Ala Thr Val Leu Gln Gln Thr Tyr His Ala His Arg Ser Asp Ala Leu | |
| 100 105 110 | |
| cag ctg ggc ctg ggg aaa cat aat tac tgc agg aac cca gac aac cgg | 384 |
| Gln Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Asn Arg | |
| 115 120 125 | |
| agg cga ccc tgg tgc tat gtg cag gtg ggc cta aag ccg ctt gtc caa | 432 |
| Arg Arg Pro Trp Cys Tyr Val Gln Val Gly Leu Lys Pro Leu Val Gln | |
| 130 135 140 | |
| gag tgc atg gtg cat gac tgc gca gat gga aaa aag ccc tcc tct cct | 480 |
| Glu Cys Met Val His Asp Cys Ala Asp Gly Lys Lys Pro Ser Ser Pro | |
| 145 150 155 160 | |
| cca gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc | 528 |
| Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg | |
| 165 170 175 | |
| ttt aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg | 576 |
| Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp | |
| 180 185 190 | |
| ttt gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg | 624 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|------|
| Phe | Ala | Ala | Ile | Tyr | Arg | Arg | His | Arg | Gly | Gly | Ser | Val | Thr | Tyr | Val | | |
| | 195 | | | | | | 200 | | | | | 205 | | | | | |
| tgt | gga | ggc | agc | ctc | atc | agc | cct | tgc | tgg | gtg | atc | agc | gcc | aca | cac | | 672 |
| Cys | Gly | Gly | Ser | Leu | Ile | Ser | Pro | Cys | Trp | Val | Ile | Ser | Ala | Thr | His | | |
| | 210 | | | | | 215 | | | | 220 | | | | | | | |
| tgc | ttc | att | gat | tac | cca | aag | aag | gag | gac | tac | atc | gtc | tac | ctg | ggc | | 720 |
| Cys | Phe | Ile | Asp | Tyr | Pro | Lys | Lys | Glu | Asp | Tyr | Ile | Val | Tyr | Leu | Gly | | |
| | 225 | | | | 230 | | | | 235 | | | | | 240 | | | |
| cgc | tca | agg | ctt | aac | tcc | aac | acg | caa | ggg | gag | atg | aag | ttt | gag | gtg | | 768 |
| Arg | Ser | Arg | Leu | Asn | Ser | Asn | Thr | Gln | Gly | Glu | Met | Lys | Phe | Glu | Val | | |
| | | | 245 | | | | | 250 | | | | | | 255 | | | |
| gaa | aac | ctc | atc | cta | cac | aag | gac | tac | agc | gct | gac | acg | ctt | gct | cac | | 816 |
| Glu | Asn | Leu | Ile | Leu | His | Lys | Asp | Tyr | Ser | Ala | Asp | Thr | Leu | Ala | His | | |
| | | 260 | | | | | 265 | | | | | | 270 | | | | |
| cac | aac | gac | att | gcc | ttg | ctg | aag | atc | cgt | tcc | aag | gag | ggc | agg | tgt | | 864 |
| His | Asn | Asp | Ile | Ala | Leu | Leu | Lys | Ile | Arg | Ser | Lys | Glu | Gly | Arg | Cys | | |
| | 275 | | | | | 280 | | | | | | 285 | | | | | |
| gcg | cag | cca | tcc | cgg | act | ata | cag | acc | atc | tgc | ctg | ccc | tcg | atg | tat | | 912 |
| Ala | Gln | Pro | Ser | Arg | Thr | Ile | Gln | Thr | Ile | Cys | Leu | Pro | Ser | Met | Tyr | | |
| | 290 | | | | 295 | | | | | 300 | | | | | | | |
| aac | gat | ccc | cag | ttt | ggc | aca | agc | tgt | gag | atc | act | ggc | ttt | gga | aaa | | 960 |
| Asn | Asp | Pro | Gln | Phe | Gly | Thr | Ser | Cys | Glu | Ile | Thr | Gly | Phe | Gly | Lys | | |
| | 305 | | | 310 | | | | 315 | | | | | | 320 | | | |
| gag | aat | tct | acc | gac | tat | ctc | tat | ccg | gag | cag | ctg | aaa | atg | act | gtt | | 1008 |
| Glu | Asn | Ser | Thr | Asp | Tyr | Leu | Tyr | Pro | Glu | Gln | Leu | Lys | Met | Thr | Val | | |
| | | | 325 | | | | | 330 | | | | | 335 | | | | |
| gtg | aag | ctg | att | tcc | cac | cgg | gag | tgt | cag | cag | ccc | cac | tac | tac | ggc | | 1056 |
| Val | Lys | Leu | Ile | Ser | His | Arg | Glu | Cys | Gln | Gln | Pro | His | Tyr | Tyr | Gly | | |
| | | 340 | | | | | 345 | | | | | 350 | | | | | |
| tct | gaa | gtc | acc | acc | aaa | atg | ctg | tgt | gct | gct | gac | cca | cag | tgg | aaa | | 1104 |
| Ser | Glu | Val | Thr | Thr | Lys | Met | Leu | Cys | Ala | Ala | Asp | Pro | Gln | Trp | Lys | | |
| | | 355 | | | | 360 | | | | | 365 | | | | | | |
| aca | gat | tcc | tgc | cag | gga | gac | tca | ggg | gga | ccc | ctc | gtc | tgt | tcc | ctc | | 1152 |
| Thr | Asp | Ser | Cys | Gln | Gly | Asp | Ser | Gly | Gly | Pro | Leu | Val | Cys | Ser | Leu | | |
| | 370 | | | | 375 | | | | | 380 | | | | | | | |
| caa | ggc | cgc | atg | act | ttg | act | gga | att | gtg | agc | tgg | ggc | cgt | gga | tgt | | 1200 |
| Gln | Gly | Arg | Met | Thr | Leu | Thr | Gly | Ile | Val | Ser | Trp | Gly | Arg | Gly | Cys | | |
| | 385 | | | | 390 | | | 395 | | | | | | 400 | | | |
| gcc | ctg | aag | gac | aag | cca | ggc | gtc | tac | acg | aga | gtc | tca | cac | ttc | tta | | 1248 |
| Ala | Leu | Lys | Asp | Lys | Pro | Gly | Val | Tyr | Thr | Arg | Val | Ser | His | Phe | Leu | | |
| | | | 405 | | | | | 410 | | | | | 415 | | | | |
| ccc | tgg | atc | cgc | agt | cac | acc | aag | gaa | gag | aat | ggc | ctg | gcc | ctc | | | 1293 |
| Pro | Trp | Ile | Arg | Ser | His | Thr | Lys | Glu | Gln | Asn | Gly | Leu | Ala | Leu | | | |
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<210> 5
 <211> 828
 <212> DNA
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<220>
 <221> CDS
 <222> (1) ... (828)
 <223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<400> 5

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| Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys | |
| 1 5 10 15 | |
| act ctg agg ccc cgc ttt aag att att ggg gga gaa ttc acc acc atc | 96 |
| Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile | |
| 20 25 30 | |
| gag aac cag ccc tgg ttt gcg gcc atc tac agg agg cac cgg ggg ggc | 144 |
| Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr Arg Arg His Arg Gly Gly | |
| 35 40 45 | |
| tct gtc acc tac gtg tgt gga ggc agc ctc atc agc cct tgc tgg gtg | 192 |
| Ser Val Thr Tyr Val Cys Gly Gly Ser Leu Ile Ser Pro Cys Trp Val | |
| 50 55 60 | |
| atc agc gcc aca cac tgc ttc att gat tac cca aag aag gag gac tac | 240 |
| Ile Ser Ala Thr His Cys Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr | |
| 65 70 75 80 | |
| atc gtc tac ctg ggt cgc tca agg ctt aac tcc aac acg caa ggg gag | 288 |
| Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu | |
| 85 90 95 | |
| atg aag ttt gag gtg gaa aac ctc atc cta cac aag gac tac agc gct | 336 |
| Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala | |
| 100 105 110 | |
| gac acg ctt gct cac cac aac gac att gcc ttg ctg aag atc cgt tcc | 384 |
| Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser | |
| 115 120 125 | |
| aag gag ggc agg tgt gcg cag cca tcc cgg act ata cag acc atc tgc | 432 |
| Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys | |
| 130 135 140 | |
| ctg ccc tcg atg tat aac gat ccc cag ttt ggc aca agc tgt gag atc | 480 |
| Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile | |
| 145 150 155 160 | |
| act ggc ttt gga aaa gag aat tct acc gac tat ctc tat ccg gag cag | 528 |
| Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln | |
| 165 170 175 | |
| ctg aaa atg act gtt gtg aag ctg att tcc cac cgg gag tgt cag cag | 576 |

| | |
|---|-----|
| Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln | |
| 180 185 190 | |
| ccc cac tac tac ggc tct gaa gtc acc acc aaa atg ctg tgt gct gct | 624 |
| Pro His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala | |
| 195 200 205 | |
| gac cca cag tgg aaa aca gat tcc tgc cag gga gac tca ggg gga ccc | 672 |
| Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro | |
| 210 215 220 | |
| ctc gtc tgt tcc ctc caa ggc cgc atg act ttg act gga att gtg agc | 720 |
| Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser | |
| 225 230 235 240 | |
| tgg ggc cgt gga tgt gcc ctg aag gac aag cca ggc gtc tac acg aga | 768 |
| Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg | |
| 245 250 255 | |
| gtc tca cac ttc tta ccc tgg atc cgc agt cac acc aag gaa gag aat | 816 |
| Val Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn | |
| 260 265 270 | |
| ggc ctg gcc ctc | 828 |
| Gly Leu Ala Leu | |
| 275 | |

<210> 6

<211> 1671

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) ... (837)

<223> Coding sequence of the surfactant protein B precursor lacking the C-terminal propeptide

<220>

<221> CDS

<222> (844) ... (1671)

<223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<400> 6

| | |
|---|-----|
| atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ctg ccc acg | 48 |
| Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr | |
| 1 5 10 15 | |
| ctc tgt ggc cca ggc act gct gcc tgg acc acc tca tcc ttg gcc tgt | 96 |
| Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys | |
| 20 25 30 | |
| gcc cag ggc cct gag ttc tgg tgc caa agc ctg gag caa gca ttg cag | 144 |
| Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln | |
| 35 40 45 | |

| | |
|---|-----|
| tgc aga gcc cta ggg cat tgc cta cag gaa gtc tgg gga cat gtg gga Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly 50 55 60 | 192 |
| gcc gat gac cta tgc caa gag tgt gag gac atc gtc cac atc ctt aac Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn 65 70 75 80 | 240 |
| aag atg gcc aag gag gcc att ttc cag gac acg atg agg aag ttc ctg Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu 85 90 95 | 288 |
| gag cag gag tgc aac gtc ctc ccc ttg aag ctg ctc atg ccc cag tgc Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys 100 105 110 | 336 |
| aac caa gtg ctt gac gac tac ttc ccc ctg gtc atc gac tac ttc cag Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln 115 120 125 | 384 |
| aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys 130 135 140 | 432 |
| tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu 145 150 155 160 | 480 |
| ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu 165 170 175 | 528 |
| gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His 180 185 190 | 576 |
| aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys 195 200 205 | 624 |
| tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys 210 215 220 | 672 |
| ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu 225 230 235 240 | 720 |
| gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile 245 250 255 | 768 |
| ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg 260 265 270 | 816 |
| ctc gtc ctc cgg tgc tcc atg aag ctt aag ccc tcc tct cct cca gaa Leu Val Leu Arg Cys Ser Met Lys Leu Lys Pro Ser Ser Pro Pro Glu 275 280 285 | 864 |

| | |
|---|------|
| gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys 290 295 300 | 912 |
| att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala 305 310 315 320 | 960 |
| gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly 325 330 335 | 1008 |
| ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe 340 345 350 | 1056 |
| att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser 355 360 365 | 1104 |
| agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn 370 375 380 | 1152 |
| ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac cac aac Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn 385 390 395 400 | 1200 |
| gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln 405 410 415 | 1248 |
| cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac gat Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp 420 425 430 | 1296 |
| ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn 435 440 445 | 1344 |
| tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys 450 455 460 | 1392 |
| ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct gaa Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu 465 470 475 480 | 1440 |
| gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa aca gat Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp 485 490 495 | 1488 |
| tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly 500 505 510 | 1536 |
| cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu | 1584 |

| 515 | 520 | 525 | |
|-------------------------|---|-----|------|
| aag gac aag cca ggc gtc | tac acg aga gtc tca cac ttc tta ccc tgg | | 1632 |
| Lys Asp Lys Pro Gly Val | Tyr Thr Arg Val Ser His Phe Leu Pro Trp | | |
| 530 | 535 | 540 | |

| | | |
|-------------------------|-----------------------------|------|
| atc cgc agt cac acc aag | gaa gag aat ggc ctg gcc ctc | 1671 |
| Ile Arg Ser His Thr Lys | Glu Gln Asn Gly Leu Ala Leu | |
| 545 | 550 | 555 |

<210> 7
 <211> 1674
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1) ... (837)
 <223> Coding sequence of the surfactant protein B precursor lacking the C-terminal propeptide

<220>
 <221> CDS
 <222> (847) ... (1674)
 <223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<400> 7

| | | |
|-----------------------------|---------------------------------|----|
| atg gct gag tca cac ctg ctg | cag tgg ctg ctg ctg ctg ccc acg | 48 |
| Met Ala Glu Ser His Leu Leu | Gln Trp Leu Leu Leu Leu Pro Thr | |
| 1 | 5 10 15 | |

| | | |
|---------------------------------|---------------------------------|----|
| ctc tgt ggc cca ggc act gct gcc | tgg acc acc tca tcc ttg gcc tgt | 96 |
| Leu Cys Gly Pro Gly Thr Ala Ala | Trp Thr Thr Ser Ser Leu Ala Cys | |
| 20 | 25 30 | |

| | | |
|---------------------------------|---------------------------------|-----|
| gcc cag ggc cct gag ttc tgg tgc | caa agc ctg gag caa gca ttg cag | 144 |
| Ala Gln Gly Pro Glu Phe Trp Cys | Gln Ser Leu Glu Gln Ala Leu Gln | |
| 35 | 40 45 | |

| | | |
|---------------------------------|---------------------------------|-----|
| tgc aga gcc cta ggg cat tgc cta | cag gaa gtc tgg gga cat gtg gga | 192 |
| Cys Arg Ala Leu Gly His Cys Leu | Gln Glu Val Trp Gly His Val Gly | |
| 50 | 55 60 | |

| | | |
|---------------------------------|---------------------------------|-----|
| gcc gat gac cta tgc caa gag tgt | gag gac atc gtc cac atc ctt aac | 240 |
| Ala Asp Asp Leu Cys Gln Glu Cys | Glu Asp Ile Val His Ile Leu Asn | |
| 65 | 70 75 80 | |

| | | |
|---------------------------------|---------------------------------|-----|
| aag atg gcc aag gag gcc att ttc | cag gac acg atg agg aag ttc ctg | 288 |
| Lys Met Ala Lys Glu Ala Ile Phe | Gln Asp Thr Met Arg Lys Phe Leu | |
| 85 | 90 95 | |

| | | |
|---------------------------------|---------------------------------|-----|
| gag cag gag tgc aac gtc ctc ccc | ttg aag ctg ctc atg ccc cag tgc | 336 |
| Glu Gln Glu Cys Asn Val Leu Pro | Leu Lys Leu Leu Met Pro Gln Cys | |
| 100 | 105 110 | |

| | | |
|---------------------------------|---------------------------------|-----|
| aac caa gtg ctt gac gac tac ttc | ccc ctg gtc atc gac tac ttc cag | 384 |
|---------------------------------|---------------------------------|-----|

| | |
|---|------|
| Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln | |
| 115 120 125 | |
| aac cag act gac tca aac ggc atc tgt atg cac ctg ggc ctg tgc aaa | 432 |
| Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys | |
| 130 135 140 | |
| tcc cgg cag cca gag cca gag cag gag cca ggg atg tca gac ccc ctg | 480 |
| Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu | |
| 145 150 155 160 | |
| ccc aaa cct ctg cgg gac cct ctg cca gac cct ctg ctg gac aag ctc | 528 |
| Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu | |
| 165 170 175 | |
| gtc ctc cct gtg ctg ccc ggg gcc ctc cag gcg agg cct ggg cct cac | 576 |
| Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His | |
| 180 185 190 | |
| aca cag gat ctc tcc gag cag caa ttc ccc att cct ctc ccc tat tgc | 624 |
| Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys | |
| 195 200 205 | |
| tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc aag | 672 |
| Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys | |
| 210 215 220 | |
| ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct ctg | 720 |
| Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu | |
| 225 230 235 240 | |
| gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc atc | 768 |
| Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile | |
| 245 250 255 | |
| ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc cgc | 816 |
| Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg | |
| 260 265 270 | |
| ctc gtc ctc cgg tgc tcc atg cag ata tct aag ccc tcc tct cct cca | 864 |
| Leu Val Leu Arg Cys Ser Met Gln Ile Ser Lys Pro Ser Ser Pro Pro | |
| 275 280 285 | |
| gaa gaa tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt | 912 |
| Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe | |
| 290 295 300 | |
| aag att att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt | 960 |
| Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe | |
| 305 310 315 320 | |
| gcg gcc atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt | 1008 |
| Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys | |
| 325 330 335 | |
| gga ggc agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc | 1056 |
| Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys | |
| 340 345 350 | |

| | |
|---|------|
| ttc att gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc | 1104 |
| Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg | |
| 355 360 365 | |
| tca agg ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa | 1152 |
| Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu | |
| 370 375 380 | |
| aac ctc atc cta cac aag gac tac agc gct gac acg ctt gct cac cac | 1200 |
| Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His | |
| 385 390 395 400 | |
| aac gac att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg | 1248 |
| Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala | |
| 405 410 415 | |
| cag cca tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac | 1296 |
| Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn | |
| 420 425 430 | |
| gat ccc cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag | 1344 |
| Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu | |
| 435 440 445 | |
| aat tct acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg | 1392 |
| Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val | |
| 450 455 460 | |
| aag ctg att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct | 1440 |
| Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser | |
| 465 470 475 480 | |
| gaa gtc acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa aca | 1488 |
| Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr | |
| 485 490 495 | |
| gat tcc tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa | 1536 |
| Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln | |
| 500 505 510 | |
| ggc cgc atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc | 1584 |
| Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala | |
| 515 520 525 | |
| ctg aag gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc | 1632 |
| Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro | |
| 530 535 540 | |
| tgg atc cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc | 1674 |
| Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu | |
| 545 550 555 | |

<210> 8

<211> 591

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (591)

<223> Coding sequence of the surfactant protein C precursor

<400> 8

| | |
|---|-----|
| atg gat gtg ggc agc aaa gag gtc ctg atg gag agc ccg ccg gac tac | 48 |
| Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr | |
| 1 5 10 15 | |
| tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac | 96 |
| Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His | |
| 20 25 30 | |
| ctg aaa cgc ctt ctt atc gtg gtg gtg gtg gtg gtc ctc atc gtc gtg | 144 |
| Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val | |
| 35 40 45 | |
| gtg att gtg gga gcc ctg ctc atg ggt ctc cac atg agc cag aaa cac | 192 |
| Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His | |
| 50 55 60 | |
| acg gag atg gtt ctg gag atg agc att ggg gcg ccg gaa gcc cag caa | 240 |
| Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln | |
| 65 70 75 80 | |
| cgc ctg gcc ctg agt gag cac ctg gtt acc act gcc acc ttc tcc atc | 288 |
| Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile | |
| 85 90 95 | |
| ggc tcc act ggc ctc gtg gtg tat gac tac cag cag ctg ctg atc gcc | 336 |
| Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala | |
| 100 105 110 | |
| tac aag cca gcc cct ggc acc tgc tgc tac atc atg aag ata gct cca | 384 |
| Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro | |
| 115 120 125 | |
| gag agc atc ccc agt ctt gag gct ctc act aga aaa gtc cac aac ttc | 432 |
| Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe | |
| 130 135 140 | |
| cag atg gaa tgc tct ctg cag gcc aag ccc gca gtg cct acg tct aag | 480 |
| Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys | |
| 145 150 155 160 | |
| ctg ggc cag gca gag ggg cga gat gca ggc tca gca ccc tcc gga ggg | 528 |
| Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly | |
| 165 170 175 | |
| gac ccg gcc ttc ctg ggc atg gcc gtg agc acc ctg tgt ggc gag gtg | 576 |
| Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val | |
| 180 185 190 | |
| ccg ctc tac tac atc | 591 |
| Pro Leu Tyr Tyr Ile | |
| 195 | |

<210> 9
<211> 174
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (174)
<223> Coding sequence of the surfactant protein C precursor lacking the C-terminal propeptide

<400> 9

| | |
|---|-----|
| atg gat gtg ggc agc aaa gag gtc ctg atg gag agc ccg ccg gac tac | 48 |
| Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr | |
| 1 5 10 15 | |
| tcc gca gct ccc cgg ggc cga ttt ggc att ccc tgc tgc cca gtg cac | 96 |
| Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His | |
| 20 25 30 | |
| ctg aaa cgc ctt ctt atc gtg gtg gtg gtg gtg gtc ctc atc gtc gtg | 144 |
| Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val | |
| 35 40 45 | |
| gtg att gtg gga gcc ctg ctc atg ggt ctc | 174 |
| Val Ile Val Gly Ala Leu Leu Met Gly Leu | |
| 50 55 | |

<210> 10
<211> 105
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1) ... (105)
<223> Coding sequence of the mature surfactant protein C

<400> 10

| | |
|---|-----|
| ttt ggc att ccc tgc tgc cca gtg cac ctg aaa cgc ctt ctt atc gtg | 48 |
| Phe Gly Ile Pro Cys Cys Pro Val His Leu Lys Arg Leu Leu Ile Val | |
| 1 5 10 15 | |
| gtg gtg gtg gtg gtc ctc atc gtc gtg gtg att gtg gga gcc ctg ctc | 96 |
| Val Val Val Val Val Leu Ile Val Val Val Ile Val Gly Ala Leu Leu | |
| 20 25 30 | |
| atg ggt ctc | 105 |
| Met Gly Leu | |
| 35 | |

<210> 11
<211> 1686
<212> DNA
<213> Homo sapiens

<220>

<221> CDS

<222> (1) ... (1686)

<223> Coding sequence of the tissue-plasminogen activator

<400> 11

| | |
|---|-----|
| atg gat gca atg aag aga ggg ctc tgc tgt gtg ctg ctg ctg tgt gga | 48 |
| Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly | |
| 1 5 10 15 | |
| gca gtc ttc gtt tgc ccc agc cag gaa atc cat gcc cga ttc aga aga | 96 |
| Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg | |
| 20 25 30 | |
| gga gcc aga tct tac caa gtg atc tgc aga gat gaa aaa acg cag atg | 144 |
| Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met | |
| 35 40 45 | |
| ata tac cag caa cat cag tca tgg ctg cgc cct gtg ctc aga agc aac | 192 |
| Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn | |
| 50 55 60 | |
| cgg gtg gaa tat tgc tgg tgc aac agt ggc agg gca cag tgc cac tca | 240 |
| Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser | |
| 65 70 75 80 | |
| gtg cct gtc aaa agt tgc agc gag cca agg tgt ttc aac ggg ggc acc | 288 |
| Val Pro Val Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr | |
| 85 90 95 | |
| tgc cag cag gcc ctg tac ttc tca gat ttc gtg tgc cag tgc ccc gaa | 336 |
| Cys Gln Gln Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu | |
| 100 105 110 | |
| gga ttt gct ggg aag tgc tgt gaa ata gat acc agg gcc acg tgc tac | 384 |
| Gly Phe Ala Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr | |
| 115 120 125 | |
| gag gac cag ggc atc agc tac agg ggc acg tgg agc aca gcg gag agt | 432 |
| Glu Asp Gln Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser | |
| 130 135 140 | |
| ggc gcc gag tgc acc aac tgg aac agc agc gcg ttg gcc cag aag ccc | 480 |
| Gly Ala Glu Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro | |
| 145 150 160 165 | |
| tac agc ggg cgg agg cca gat gcc atc agg ctg ggc ctg ggg aac cac | 528 |
| Tyr Ser Gly Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His | |
| 170 175 180 | |
| aac tac tgc aga aac cca gat cga gac tca aag ccc tgg tgc tac gtc | 576 |
| Asn Tyr Cys Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val | |
| 185 190 195 | |
| ttt aag gcg ggg aag tac agc tca gag ttc tgc agc acc cct gcc tgc | 624 |
| Phe Lys Ala Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys | |
| 200 205 205 | |

| | |
|---|------|
| tct gag gga aac agt gac tgc tac ttt ggg aat ggg tca gcc tac cgt Ser Glu Gly Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg 210 215 220 | 672 |
| ggc acg cac agc ctc acc gag tgc ggt gcc tcc tgc ctc ccg tgg aat Gly Thr His Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn 225 230 235 240 | 720 |
| tcc atg atc ctg ata ggc aag gtt tac aca gca cag aac ccc agt gcc Ser Met Ile Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala 245 250 255 | 768 |
| cag gca ctg ggc ctg ggc aaa cat aat tac tgc cgg aat cct gat ggg Gln Ala Leu Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly 260 265 270 | 816 |
| gat gcc aag ccc tgg tgc cac gtg ctg aag aac cgc agg ctg acg tgg Asp Ala Lys Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp 275 280 285 | 864 |
| gag tac tgt gat gtg ccc tcc tgc tcc acc tgc ggc ctg aga cag tac Glu Tyr Cys Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr 290 295 300 | 912 |
| agc cag cct cag ttt cgc atc aaa gga ggg ctc ttc gcc gac atc gcc Ser Gln Pro Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala 305 310 315 320 | 960 |
| tcc cac ccc tgg cag gct gcc atc ttt gcc aag cac agg agg tgc ccc Ser His Pro Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro 325 330 335 | 1008 |
| gga gag cgg ttc ctg tgc ggg ggc ata ctc atc agc tcc tgc tgg att Gly Glu Arg Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile 340 345 350 | 1056 |
| ctc tct gcc gcc cac tgc ttc cag gag agg ttt ccg ccc cac cac ctg Leu Ser Ala Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu 355 360 365 | 1104 |
| acg gtg atc ttg ggc aga aca tac cgg gtg gtc cct ggc gag gag gag Thr Val Ile Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu 370 375 380 | 1152 |
| cag aaa ttt gaa gtc gaa aaa tac att gtc cat aag gaa ttc gat gat Gln Lys Phe Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp 385 390 395 400 | 1200 |
| gac act tac gac aat gac att gcg ctg ctg cag ctg aaa tcg gat tcg Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser 405 410 415 | 1248 |
| tcc cgc tgt gcc cag gag agc agc gtg gtc cgc act gtg tgc ctt ccc Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro 420 425 430 | 1296 |
| ccg gcg gac ctg cag ctg ccg gac tgg acg gag tgt gag ctc tcc ggc Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly | 1344 |

| 435 | 440 | 445 | |
|---|-----|-----|------|
| tac ggc aag cat gag gcc ttg tct cct ttc tat tgc gag cgg ctg aag | | | 1392 |
| Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys | | | |
| 450 | 455 | 460 | |
| gag gct cat gtc aga ctg tac cca tcc agc cgc tgc aca tca caa cat | | | 1440 |
| Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His | | | |
| 465 | 470 | 475 | 480 |
| tta ctt aac aga aca gtc acc gac aac atg ctg tgt gct gga gac act | | | 1488 |
| Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr | | | |
| | 485 | 490 | 495 |
| cgg agc ggc ggg ccc cag gca aac ttg cac gac gcc tgc cag ggc gat | | | 1536 |
| Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp | | | |
| | 500 | 505 | 510 |
| tgc gga ggc ccc ctg gtg tgt ctg aac gat ggc cgc atg act ttg gtg | | | 1584 |
| Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val | | | |
| | 515 | 520 | 525 |
| ggc atc atc agc tgg ggc ctg ggc tgt gga cag aag gat gtc ccg ggt | | | 1632 |
| Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly | | | |
| | 530 | 535 | 540 |
| gtg tac acc aag gtt acc aac tac cta gac tgg att cgt gac aac atg | | | 1680 |
| Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met | | | |
| | 545 | 550 | 555 |
| cga ccg | | | 1686 |
| Arg Pro | | | |

<210> 12
 <211> 1158
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> sig_peptide
 <222> (1) ... (69)
 <223> Signal sequence of the surfactant protein B

<220>
 <221> CDS
 <222> (76) ... (312)
 <223> Coding sequence of the mature surfactant protein B

<220>
 <221> CDS
 <222> (313) ... (1140)
 <223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<220>
 <221> CDS
 <222> (1141) ... (1158)
 <223> Hexahistidin affinity tag

<400> 12

| | |
|---|-----|
| atg gct gag tca cac ctg ctg cag tgg ctg ctg ctg ctg ccc acg | 48 |
| Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr | |
| 1 5 10 15 | |
| ctc tgt ggc cca ggc act gct gcc tgg ttc ccc att cct ctc ccc tat | 96 |
| Leu Cys Gly Pro Gly Thr Ala Ala Trp Phe Pro Ile Pro Leu Pro Tyr | |
| 20 25 30 | |
| tgc tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att ccc | 144 |
| Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro | |
| 35 40 45 | |
| aag ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta cct | 192 |
| Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro | |
| 50 55 60 | |
| ctg gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc gtc | 240 |
| Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val | |
| 65 70 75 80 | |
| atc ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc tgc | 288 |
| Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys | |
| 85 90 95 | |
| cgc ctc gtc ctc cgg tgc tcc atg aag ccc tcc tct cct cca gaa gaa | 336 |
| Arg Leu Val Leu Arg Cys Ser Met Lys Pro Ser Ser Pro Pro Glu Glu | |
| 100 105 110 | |
| tta aaa ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag att | 384 |
| Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile | |
| 115 120 125 | |
| att ggg gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg gcc | 432 |
| Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala | |
| 130 135 140 | |
| atc tac agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga ggc | 480 |
| Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly | |
| 145 150 155 160 | |
| agc ctc atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc att | 528 |
| Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile | |
| 165 170 175 | |
| gat tac cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca agg | 576 |
| Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg | |
| 180 185 190 | |
| ctt aac tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac ctc | 624 |
| Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu | |
| 195 200 205 | |
| atc cta cac aag gac tac agc gct gac acg ctt gct cac cac aac gac | 672 |
| Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp | |
| 210 215 220 | |

| | |
|---|------|
| att gcc ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag cca Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro 225 230 235 240 | 720 |
| tcc cgg act ata cag acc atc tgc ctg ccc tcg atg tat aac gat ccc Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro 245 250 255 | 768 |
| cag ttt ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat tct Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser 260 265 270 | 816 |
| acc gac tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag ctg Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu 275 280 285 | 864 |
| att tcc cac cgg gag tgt cag cag ccc cac tac tac ggc tct gaa gtc Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val 290 295 300 | 912 |
| acc acc aaa atg ctg tgt gct gct gac cca cag tgg aaa aca gat tcc Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser 305 310 315 320 | 960 |
| tgc cag gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc cgc Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg 325 330 335 | 1008 |
| atg act ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg aag Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys 340 345 350 | 1056 |
| gac aag cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg atc Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile 355 360 365 | 1104 |
| cgc agt cac acc aag gaa gag aat ggc ctg gcc ctc cat cat cat cat Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu His His His His 370 375 380 | 1152 |
| cat cat His His 385 | 1158 |

<210> 13

<211> 1149

<212> DNA

<213> Artificial Sequence

<220>

<221> sig_peptide

<222> (1) ... (60)

<223> Signal sequence of the urokinase plasminogen activator

<220>

<221> CDS

<222> (67) ... (894)

<223> Coding sequence of the low molecular weight two-chain urokinase-plasminogen activator

<220>

<221> CDS

<222> (895) ... (1131)

<223> Coding sequence of the mature surfactant protein B

<220>

<221> CDS

<222> (1132) ... (1149)

<223> Hexahistidin affinity tag

<400> 13

| | |
|---|-----|
| atg aga gcc ctg ctg gcg cgc ctg ctt ctc tgc gtc ctg gtc gtg agc | 48 |
| Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser | |
| 1 5 10 15 | |
| gac tcc aaa ggc agc aat aag ccc tcc tct cct cca gaa gaa tta aaa | 96 |
| Asp Ser Lys Gly Ser Asn Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys | |
| 20 25 30 | |
| ttt cag tgt ggc caa aag act ctg agg ccc cgc ttt aag att att ggg | 144 |
| Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly | |
| 35 40 45 | |
| gga gaa ttc acc acc atc gag aac cag ccc tgg ttt gcg gcc atc tac | 192 |
| Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr | |
| 50 55 60 | |
| agg agg cac cgg ggg ggc tct gtc acc tac gtg tgt gga ggc agc ctc | 240 |
| Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser Leu | |
| 65 70 75 80 | |
| atc agc cct tgc tgg gtg atc agc gcc aca cac tgc ttc att gat tac | 288 |
| Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile Asp Tyr | |
| 85 90 95 | |
| cca aag aag gag gac tac atc gtc tac ctg ggt cgc tca agg ctt aac | 336 |
| Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn | |
| 100 105 110 | |
| tcc aac acg caa ggg gag atg aag ttt gag gtg gaa aac ctc atc cta | 384 |
| Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu | |
| 115 120 125 | |
| cac aag gac tac agc gct gac acg ctt gct cac cac aac gac att gcc | 432 |
| His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala | |
| 130 135 140 | |
| ttg ctg aag atc cgt tcc aag gag ggc agg tgt gcg cag cca tcc cgg | 480 |
| Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg | |
| 145 150 155 160 | |
| act ata cag acc atc tgc ctg ccc tcg atg tat aac gat ccc cag ttt | 528 |
| Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe | |
| 165 170 175 | |

| | |
|---|------|
| ggc aca agc tgt gag atc act ggc ttt gga aaa gag aat tct acc gac Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp 180 185 190 | 576 |
| tat ctc tat ccg gag cag ctg aaa atg act gtt gtg aag ctg att tcc Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile Ser 195 200 205 | 624 |
| cac cgg gag tgt cag cag ccc cac tac tac ggc tct gaa gtc acc acc His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr 210 215 220 | 672 |
| aaa atg ctg tgt gct gct gac cca cag tgg aaa aca gat tcc tgc cag Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln 225 230 235 240 | 720 |
| gga gac tca ggg gga ccc ctc gtc tgt tcc ctc caa ggc cgc atg act Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr 245 250 255 | 768 |
| ttg act gga att gtg agc tgg ggc cgt gga tgt gcc ctg aag gac aag Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys 260 265 270 | 816 |
| cca ggc gtc tac acg aga gtc tca cac ttc tta ccc tgg atc cgc agt Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg Ser 275 280 285 | 864 |
| cac acc aag gaa gag aat ggc ctg gcc ctc ttc ccc att cct ctc ccc His Thr Lys Glu Gln Asn Gly Leu Ala Leu Phe Pro Ile Pro Leu Pro 290 295 300 | 912 |
| tat tgc tgg ctc tgc agg gct ctg atc aag cgg atc caa gcc atg att Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile 305 310 315 320 | 960 |
| ccc aag ggt gcg cta gct gtg gca gtg gcc cag gtg tgc cgc gtg gta Pro Lys Gly Ala Leu Ala Val Ala Val Gln Val Cys Arg Val Val 325 330 335 | 1008 |
| cct ctg gtg gcg ggc ggc atc tgc cag tgc ctg gct gag cgc tac tcc Pro Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser 340 345 350 | 1056 |
| gtc atc ctg ctc gac acg ctg ctg ggc cgc atg ctg ccc cag ctg gtc Val Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val 355 360 365 | 1104 |
| tgc cgc ctc gtc ctc cgg tgc tcc atg cat cat cat cat cat cat Cys Arg Leu Val Leu Arg Cys Ser Met His His His His His His 370 375 380 | 1149 |

<210> 14

<211> 381

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (381)

<223> Surfactant protein B precursor

<400> 14

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Ala | Glu | Ser | His | Leu | Leu | Gln | Trp | Leu | Leu | Leu | Leu | Leu | Pro | Thr | |
| 1 | | | | 5 | | | | 10 | | | | | | 15 | | |
| Leu | Cys | Gly | Pro | Gly | Thr | Ala | Ala | Trp | Thr | Thr | Ser | Ser | Leu | Ala | Cys | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| Ala | Gln | Gly | Pro | Glu | Phe | Trp | Cys | Gln | Ser | Leu | Glu | Gln | Ala | Leu | Gln | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| Cys | Arg | Ala | Leu | Gly | His | Cys | Leu | Gln | Glu | Val | Trp | Gly | His | Val | Gly | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| Ala | Asp | Asp | Leu | Cys | Gln | Glu | Cys | Glu | Asp | Ile | Val | His | Ile | Leu | Asn | |
| | 65 | | | | 70 | | | | | 75 | | | | | 80 | |
| Lys | Met | Ala | Lys | Glu | Ala | Ile | Phe | Gln | Asp | Thr | Met | Arg | Lys | Phe | Leu | |
| | | | 85 | | | | | | 90 | | | | | 95 | | |
| Glu | Gln | Glu | Cys | Asn | Val | Leu | Pro | Leu | Lys | Leu | Leu | Met | Pro | Gln | Cys | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| Asn | Gln | Val | Leu | Asp | Asp | Tyr | Phe | Pro | Leu | Val | Ile | Asp | Tyr | Phe | Gln | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| Asn | Gln | Thr | Asp | Ser | Asn | Gly | Ile | Cys | Met | His | Leu | Gly | Leu | Cys | Lys | |
| | | 130 | | | | 135 | | | | | 140 | | | | | |
| Ser | Arg | Gln | Pro | Glu | Pro | Glu | Gln | Glu | Pro | Gly | Met | Ser | Asp | Pro | Leu | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| Pro | Lys | Pro | Leu | Arg | Asp | Pro | Leu | Pro | Asp | Pro | Leu | Leu | Asp | Lys | Leu | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| Val | Leu | Pro | Val | Leu | Pro | Gly | Ala | Leu | Gln | Ala | Arg | Pro | Gly | Pro | His | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| Thr | Gln | Asp | Leu | Ser | Glu | Gln | Gln | Phe | Pro | Ile | Pro | Leu | Pro | Tyr | Cys | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| Trp | Leu | Cys | Arg | Ala | Leu | Ile | Lys | Arg | Ile | Gln | Ala | Met | Ile | Pro | Lys | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| Gly | Ala | Leu | Ala | Val | Ala | Val | Ala | Gln | Val | Cys | Arg | Val | Val | Pro | Leu | |
| 225 | | | | 230 | | | | | | 235 | | | | 240 | | |
| Val | Ala | Gly | Gly | Ile | Cys | Gln | Cys | Leu | Ala | Glu | Arg | Tyr | Ser | Val | Ile | |
| | | | 245 | | | | | 250 | | | | | | 255 | | |
| Leu | Leu | Asp | Thr | Leu | Leu | Gly | Arg | Met | Leu | Pro | Gln | Leu | Val | Cys | Arg | |
| | | | 260 | | | | 265 | | | | | | 270 | | | |
| Leu | Val | Leu | Arg | Cys | Ser | Met | Asp | Asp | Ser | Ala | Gly | Pro | Arg | Ser | Pro | |

| | | |
|---|-----|---------|
| 275 | 280 | 285 |
| Thr Gly Glu Trp Leu Pro Arg Asp Ser Glu Cys His Leu Cys Met Ser | | |
| 290 | 295 | 300 |
| Val Thr Thr Gln Ala Gly Asn Ser Ser Glu Gln Ala Ile Pro Gln Ala | | |
| 305 | 310 | 315 320 |
| Met Leu Gln Ala Cys Val Gly Ser Trp Leu Asp Arg Glu Lys Cys Lys | | |
| | 325 | 330 335 |
| Gln Phe Val Glu Gln His Thr Pro Gln Leu Leu Thr Leu Val Pro Arg | | |
| | 340 | 345 350 |
| Gly Trp Asp Ala His Thr Thr Cys Gln Ala Leu Gly Val Cys Gly Thr | | |
| | 355 | 360 365 |
| Met Ser Ser Pro Leu Gln Cys Ile His Ser Pro Asp Leu | | |
| | 370 | 375 380 |

<210> 15
 <211> 279
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> PEPTIDE
 <222> (1) ... (279)
 <223> Surfactant protein B precursor lacking the C-terminal propeptide

 <400> 15

| | | |
|---|-----|----------|
| Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Pro Thr | | |
| 1 | 5 | 10 15 |
| Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys | | |
| | 20 | 25 30 |
| Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln | | |
| | 35 | 40 45 |
| Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly | | |
| | 50 | 55 60 |
| Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn | | |
| | 65 | 70 75 80 |
| Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu | | |
| | 85 | 90 95 |
| Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys | | |
| | 100 | 105 110 |
| Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln | | |
| | 115 | 120 125 |
| Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys | | |
| | 130 | 135 140 |

Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu
 145 150 155 160
 Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu
 165 170 175
 Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His
 180 185 190
 Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys
 195 200 205
 Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys
 210 215 220
 Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu
 225 230 235 240
 Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile
 245 250 255
 Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg
 260 265 270
 Leu Val Leu Arg Cys Ser Met
 275

<210> 16
 <211> 79
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1) ... (79)
 <223> Mature surfactant protein B

<400> 16

Phe Pro Ile Pro Leu Pro Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys
 1 5 10 15
 Arg Ile Gln Ala Met Ile Pro Lys Gly Ala Leu Ala Val Ala Val Ala
 20 25 30
 Gln Val Cys Arg Val Val Pro Leu Val Ala Gly Gly Ile Cys Gln Cys
 35 40 45
 Leu Ala Glu Arg Tyr Ser Val Ile Leu Leu Asp Thr Leu Leu Gly Arg
 50 55 60
 Met Leu Pro Gln Leu Val Cys Arg Leu Val Leu Arg Cys Ser Met
 65 70 75

<210> 17
 <211> 431

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (431)

<223> Single-chain urokinase-plasminogen activator

<400> 17

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Met | Arg | Ala | Leu | Leu | Ala | Arg | Leu | Leu | Leu | Cys | Val | Leu | Val | Val | Ser | |
| 1 | | | | 5 | | | | | 10 | | | | | | 15 | |
| Asp | Ser | Lys | Gly | Ser | Asn | Glu | Leu | His | Gln | Val | Pro | Ser | Asn | Cys | Asp | |
| | | | 20 | | | | | 25 | | | | | | 30 | | |
| Cys | Leu | Asn | Gly | Gly | Thr | Cys | Val | Ser | Asn | Lys | Tyr | Phe | Ser | Asn | Ile | |
| | | 35 | | | | | 40 | | | | | | 45 | | | |
| His | Trp | Cys | Asn | Cys | Pro | Lys | Lys | Phe | Gly | Gly | Gln | His | Cys | Glu | Ile | |
| | 50 | | | | | | 55 | | | | | 60 | | | | |
| Asp | Lys | Ser | Lys | Thr | Cys | Tyr | Glu | Gly | Asn | Gly | His | Phe | Tyr | Arg | Gly | |
| | 65 | | | | | 70 | | | | 75 | | | | | 80 | |
| Lys | Ala | Ser | Thr | Asp | Thr | Met | Gly | Arg | Pro | Cys | Leu | Pro | Trp | Asn | Ser | |
| | | | | 85 | | | | | 90 | | | | | | 95 | |
| Ala | Thr | Val | Leu | Gln | Gln | Thr | Tyr | His | Ala | His | Arg | Ser | Asp | Ala | Leu | |
| | | | 100 | | | | | 105 | | | | | | 110 | | |
| Gln | Leu | Gly | Leu | Gly | Lys | His | Asn | Tyr | Cys | Arg | Asn | Pro | Asp | Asn | Arg | |
| | | 115 | | | | | 120 | | | | | | 125 | | | |
| Arg | Arg | Pro | Trp | Cys | Tyr | Val | Gln | Val | Gly | Leu | Lys | Pro | Leu | Val | Gln | |
| | | 130 | | | | | 135 | | | | | 140 | | | | |
| Glu | Cys | Met | Val | His | Asp | Cys | Ala | Asp | Gly | Lys | Lys | Pro | Ser | Ser | Pro | |
| | 145 | | | | 150 | | | | | 155 | | | | | 160 | |
| Pro | Glu | Glu | Leu | Lys | Phe | Gln | Cys | Gly | Gln | Lys | Thr | Leu | Arg | Pro | Arg | |
| | | | | 165 | | | | | 170 | | | | | | 175 | |
| Phe | Lys | Ile | Ile | Gly | Gly | Glu | Phe | Thr | Thr | Ile | Glu | Asn | Gln | Pro | Trp | |
| | | | 180 | | | | | 185 | | | | | | 190 | | |
| Phe | Ala | Ala | Ile | Tyr | Arg | Arg | His | Arg | Gly | Gly | Ser | Val | Thr | Tyr | Val | |
| | | 195 | | | | | 200 | | | | | | 205 | | | |
| Cys | Gly | Gly | Ser | Leu | Ile | Ser | Pro | Cys | Trp | Val | Ile | Ser | Ala | Thr | His | |
| | | 210 | | | | | 215 | | | | | 220 | | | | |
| Cys | Phe | Ile | Asp | Tyr | Pro | Lys | Lys | Glu | Asp | Tyr | Ile | Val | Tyr | Leu | Gly | |
| | 225 | | | | | 230 | | | | 235 | | | | | 240 | |
| Arg | Ser | Arg | Leu | Asn | Ser | Asn | Thr | Gln | Gly | Glu | Met | Lys | Phe | Glu | Val | |
| | | | | 245 | | | | | | 250 | | | | | 255 | |
| Glu | Asn | Leu | Ile | Leu | His | Lys | Asp | Tyr | Ser | Ala | Asp | Thr | Leu | Ala | His | |

Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu
 85 90 95
 Met Lys Phe Glu Val Glu Asn Leu Ile Leu His Lys Asp Tyr Ser Ala
 100 105 110
 Asp Thr Leu Ala His His Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser
 115 120 125
 Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys
 130 135 140
 Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile
 145 150 155 160
 Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln
 165 170 175
 Leu Lys Met Thr Val Val Lys Leu Ile Ser His Arg Glu Cys Gln Gln
 180 185 190
 Pro His Tyr Tyr Gly Ser Glu Val Thr Thr Lys Met Leu Cys Ala Ala
 195 200 205
 Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro
 210 215 220
 Leu Val Cys Ser Leu Gln Gly Arg Met Thr Leu Thr Gly Ile Val Ser
 225 230 235 240
 Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg
 245 250 255
 Val Ser His Phe Leu Pro Trp Ile Arg Ser His Thr Lys Glu Gln Asn
 260 265 270
 Gly Leu Ala Leu
 275

<210> 19

<211> 557

<212> PRT

<213> Artificial Sequence

<220>

<221> PEPTIDE

<222> (1) ... (279)

<223> Surfactant protein B precursor lacking the C-terminal propeptide

<220>

<221> PEPTIDE

<222> (282) ... (577)

<223> Low molecular weight two-chain urokinase-plasminogen activator

<400> 19

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr

| | | | |
|-------------|---------------------|-------------------------|---------------------|
| 1 | 5 | 10 | 15 |
| Leu Cys Gly | Pro Gly Thr | Ala Ala Trp Thr Thr | Ser Ser Leu Ala Cys |
| 20 | | 25 | 30 |
| Ala Gln Gly | Pro Glu Phe Trp | Cys Gln Ser Leu Glu Gln | Ala Leu Gln |
| 35 | | 40 | 45 |
| Cys Arg Ala | Leu Gly His Cys | Leu Gln Glu Val Trp | Gly His Val Gly |
| 50 | | 55 | 60 |
| Ala Asp Asp | Leu Cys Gln Glu | Cys Glu Asp Ile Val | His Ile Leu Asn |
| 65 | | 70 | 75 |
| Lys Met Ala | Lys Glu Ala Ile Phe | Gln Asp Thr Met Arg | Lys Phe Leu |
| | 85 | 90 | 95 |
| Glu Gln Glu | Cys Asn Val Leu Pro | Leu Lys Leu Leu Met | Pro Gln Cys |
| | 100 | 105 | 110 |
| Asn Gln Val | Leu Asp Asp Tyr Phe | Pro Leu Val Ile Asp | Tyr Phe Gln |
| | 115 | 120 | 125 |
| Asn Gln Thr | Asp Ser Asn Gly Ile | Cys Met His Leu Gly | Leu Cys Lys |
| | 130 | 135 | 140 |
| Ser Arg Gln | Pro Glu Glu Glu Pro | Gly Met Ser Asp Pro | Leu |
| 145 | | 150 | 155 |
| Pro Lys Pro | Leu Arg Asp Pro | Leu Pro Asp Pro | Leu Leu Asp Lys Leu |
| | 165 | 170 | 175 |
| Val Leu Pro | Val Leu Pro Gly Ala | Leu Gln Ala Arg Pro | Gly Pro His |
| | 180 | 185 | 190 |
| Thr Gln Asp | Leu Ser Glu Gln Gln | Phe Pro Ile Pro Leu | Pro Tyr Cys |
| | 195 | 200 | 205 |
| Trp Leu Cys | Arg Ala Leu Ile Lys | Arg Ile Gln Ala Met | Ile Pro Lys |
| | 210 | 215 | 220 |
| Gly Ala Leu | Ala Val Ala Val Ala | Gln Val Cys Arg Val | Val Pro Leu |
| 225 | | 230 | 235 |
| Val Ala Gly | Gly Ile Cys Gln Cys | Leu Ala Glu Arg Tyr | Ser Val Ile |
| | 245 | 250 | 255 |
| Leu Leu Asp | Thr Leu Leu Gly Arg | Met Leu Pro Gln Leu | Val Cys Arg |
| | 260 | 265 | 270 |
| Leu Val Leu | Arg Cys Ser Met Lys | Leu Lys Pro Ser Ser | Pro Pro Glu |
| | 275 | 280 | 285 |
| Glu Leu Lys | Phe Gln Cys Gly Gln | Lys Thr Leu Arg Pro | Arg Phe Lys |
| | 290 | 295 | 300 |
| Ile Ile Gly | Gly Glu Phe Thr Thr | Ile Glu Asn Gln Pro | Trp Phe Ala |
| 305 | | 310 | 315 |
| | | | 320 |

<223> Low molecular weight two-chain urokinase-plasminogen activator

<400> 20

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr
1 5 10 15

Leu Cys Gly Pro Gly Thr Ala Ala Trp Thr Thr Ser Ser Leu Ala Cys
20 25 30

Ala Gln Gly Pro Glu Phe Trp Cys Gln Ser Leu Glu Gln Ala Leu Gln
35 40 45

Cys Arg Ala Leu Gly His Cys Leu Gln Glu Val Trp Gly His Val Gly
50 55 60

Ala Asp Asp Leu Cys Gln Glu Cys Glu Asp Ile Val His Ile Leu Asn
65 70 75 80

Lys Met Ala Lys Glu Ala Ile Phe Gln Asp Thr Met Arg Lys Phe Leu
85 90 95

Glu Gln Glu Cys Asn Val Leu Pro Leu Lys Leu Leu Met Pro Gln Cys
100 105 110

Asn Gln Val Leu Asp Asp Tyr Phe Pro Leu Val Ile Asp Tyr Phe Gln
115 120 125

Asn Gln Thr Asp Ser Asn Gly Ile Cys Met His Leu Gly Leu Cys Lys
130 135 140

Ser Arg Gln Pro Glu Pro Glu Gln Glu Pro Gly Met Ser Asp Pro Leu
145 150 155 160

Pro Lys Pro Leu Arg Asp Pro Leu Pro Asp Pro Leu Leu Asp Lys Leu
165 170 175

Val Leu Pro Val Leu Pro Gly Ala Leu Gln Ala Arg Pro Gly Pro His
180 185 190

Thr Gln Asp Leu Ser Glu Gln Gln Phe Pro Ile Pro Leu Pro Tyr Cys
195 200 205

Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro Lys
210 215 220

Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro Leu
225 230 235 240

Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val Ile
245 250 255

Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys Arg
260 265 270

Leu Val Leu Arg Cys Ser Met Gln Ile Ser Lys Pro Ser Ser Pro Pro
275 280 285

Glu Glu Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe

| 290 | 295 | 300 |
|--|-----|-----|
| Lys Ile Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe 305 310 315 320 | | |
| Ala Ala Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys 325 330 335 | | |
| Gly Gly Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys 340 345 350 | | |
| Phe Ile Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg 355 360 365 | | |
| Ser Arg Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu 370 375 380 | | |
| Asn Leu Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His 385 390 395 400 | | |
| Asn Asp Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala 405 410 415 | | |
| Gln Pro Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn 420 425 430 | | |
| Asp Pro Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu 435 440 445 | | |
| Asn Ser Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val 450 455 460 | | |
| Lys Leu Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser 465 470 475 480 | | |
| Glu Val Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr 485 490 495 | | |
| Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln 500 505 510 | | |
| Gly Arg Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala 515 520 525 | | |
| Leu Lys Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro 530 535 540 | | |
| Trp Ile Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu 545 550 555 | | |

<210> 21

<211> 197

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) (197)

<223> Surfactant protein C precursor

<400> 21

Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr
1 5 10 15

Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His
20 25 30

Leu Lys Arg Leu Leu Ile Val Val Val Val Val Leu Ile Val Val
35 40 45

Val Ile Val Gly Ala Leu Leu Met Gly Leu His Met Ser Gln Lys His
50 55 60

Thr Glu Met Val Leu Glu Met Ser Ile Gly Ala Pro Glu Ala Gln Gln
65 70 75 80

Arg Leu Ala Leu Ser Glu His Leu Val Thr Thr Ala Thr Phe Ser Ile
85 90 95

Gly Ser Thr Gly Leu Val Val Tyr Asp Tyr Gln Gln Leu Leu Ile Ala
100 105 110

Tyr Lys Pro Ala Pro Gly Thr Cys Cys Tyr Ile Met Lys Ile Ala Pro
115 120 125

Glu Ser Ile Pro Ser Leu Glu Ala Leu Thr Arg Lys Val His Asn Phe
130 135 140

Gln Met Glu Cys Ser Leu Gln Ala Lys Pro Ala Val Pro Thr Ser Lys
145 150 155 160

Leu Gly Gln Ala Glu Gly Arg Asp Ala Gly Ser Ala Pro Ser Gly Gly
165 170 175

Asp Pro Ala Phe Leu Gly Met Ala Val Ser Thr Leu Cys Gly Glu Val
180 185 190

Pro Leu Tyr Tyr Ile
195

<210> 22

<211> 58

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (58)

<223> Surfactant protein C precursor lacking the C-terminal propeptide

<400> 22

Met Asp Val Gly Ser Lys Glu Val Leu Met Glu Ser Pro Pro Asp Tyr
1 5 10 15

Ser Ala Ala Pro Arg Gly Arg Phe Gly Ile Pro Cys Cys Pro Val His
20 25 30

Leu Lys Arg Leu Leu Ile Val Val Val Val Val Val Leu Ile Val Val
35 40 45

Val Ile Val Gly Ala Leu Leu Met Gly Leu
50 55

<210> 23

<211> 35

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (35)

<223> Mature surfactant protein C

<400> 23

Phe Gly Ile Pro Cys Cys Pro Val His Leu Lys Arg Leu Leu Ile Val
1 5 10 15

Val Val Val Val Val Leu Ile Val Val Val Ile Val Gly Ala Leu Leu
20 25 30

Met Gly Leu
35

<210> 24

<211> 562

<212> DNA

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1) ... (562)

<223> Tissue-plasminogen activator

<400> 24

Met Asp Ala Met Lys Arg Gly Leu Cys Cys Val Leu Leu Leu Cys Gly
1 5 10 15

Ala Val Phe Val Ser Pro Ser Gln Glu Ile His Ala Arg Phe Arg Arg
20 25 30

Gly Ala Arg Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met
35 40 45

Ile Tyr Gln Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn
50 55 60

Arg Val Glu Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser
65 70 75 80

| | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Pro | Val | Lys | Ser | Cys | Ser | Glu | Pro | Arg | Cys | Phe | Asn | Gly | Gly | Thr | 85 | 90 | 95 |
| Cys | Gln | Gln | Ala | Leu | Tyr | Phe | Ser | Asp | Phe | Val | Cys | Gln | Cys | Pro | Glu | 100 | 105 | 110 |
| Gly | Phe | Ala | Gly | Lys | Cys | Cys | Glu | Ile | Asp | Thr | Arg | Ala | Thr | Cys | Tyr | 115 | 120 | 125 |
| Glu | Asp | Gln | Gly | Ile | Ser | Tyr | Arg | Gly | Thr | Trp | Ser | Thr | Ala | Glu | Ser | 130 | 135 | 140 |
| Gly | Ala | Glu | Cys | Thr | Asn | Trp | Asn | Ser | Ser | Ala | Leu | Ala | Gln | Lys | Pro | 145 | 150 | 160 |
| Tyr | Ser | Gly | Arg | Arg | Pro | Asp | Ala | Ile | Arg | Leu | Gly | Leu | Gly | Asn | His | 170 | 175 | 180 |
| Asn | Tyr | Cys | Arg | Asn | Pro | Asp | Arg | Asp | Ser | Lys | Pro | Trp | Cys | Tyr | Val | 185 | 190 | 195 |
| Phe | Lys | Ala | Gly | Lys | Tyr | Ser | Ser | Glu | Phe | Cys | Ser | Thr | Pro | Ala | Cys | 200 | 205 | 205 |
| Ser | Glu | Gly | Asn | Ser | Asp | Cys | Tyr | Phe | Gly | Asn | Gly | Ser | Ala | Tyr | Arg | 210 | 215 | 220 |
| Gly | Thr | His | Ser | Leu | Thr | Glu | Ser | Gly | Ala | Ser | Cys | Leu | Pro | Trp | Asn | 225 | 230 | 235 |
| Ser | Met | Ile | Leu | Ile | Gly | Lys | Val | Tyr | Thr | Ala | Gln | Asn | Pro | Ser | Ala | 245 | 250 | 255 |
| Gln | Ala | Leu | Gly | Leu | Gly | Lys | His | Asn | Tyr | Cys | Arg | Asn | Pro | Asp | Gly | 260 | 265 | 270 |
| Asp | Ala | Lys | Pro | Trp | Cys | His | Val | Leu | Lys | Asn | Arg | Arg | Leu | Thr | Trp | 275 | 280 | 285 |
| Glu | Tyr | Cys | Asp | Val | Pro | Ser | Cys | Ser | Thr | Cys | Gly | Leu | Arg | Gln | Tyr | 290 | 295 | 300 |
| Ser | Gln | Pro | Gln | Phe | Arg | Ile | Lys | Gly | Gly | Leu | Phe | Ala | Asp | Ile | Ala | 305 | 310 | 315 |
| Ser | His | Pro | Trp | Gln | Ala | Ala | Ile | Phe | Ala | Lys | His | Arg | Arg | Ser | Pro | 325 | 330 | 335 |
| Gly | Glu | Arg | Phe | Leu | Cys | Gly | Gly | Ile | Leu | Ile | Ser | Ser | Cys | Trp | Ile | 340 | 345 | 350 |
| Leu | Ser | Ala | Ala | His | Cys | Phe | Gln | Glu | Arg | Phe | Pro | Pro | His | His | Leu | 355 | 360 | 365 |
| Thr | Val | Ile | Leu | Gly | Arg | Thr | Tyr | Arg | Val | Val | Pro | Gly | Glu | Glu | Glu | 370 | 375 | 380 |
| Gln | Lys | Phe | Glu | Val | Glu | Lys | Tyr | Ile | Val | His | Lys | Glu | Phe | Asp | Asp | 385 | 390 | 395 |

Asp Thr Tyr Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser
 405 410 415
 Ser Arg Cys Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro
 420 425 430
 Pro Ala Asp Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly
 435 440 445
 Tyr Gly Lys His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys
 450 455 460
 Glu Ala His Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His
 465 470 475 480
 Leu Leu Asn Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr
 485 490 495
 Arg Ser Gly Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp
 500 505 510
 Ser Gly Gly Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val
 515 520 525
 Gly Ile Ile Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly
 530 535 540
 Val Tyr Thr Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met
 545 550 555 560
 Arg Pro

<210> 25
 <211> 386
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> SIGNAL
 <222> (1) ... (23)
 <223> Signal sequence of the surfactant protein B

<220>
 <221> PEPTIDE
 <222> (26) ... (104)
 <223> Mature surfactant protein B

<220>
 <221> PEPTIDE
 <222> (105) ... (380)
 <223> Low molecular weight two-chain urokinase-plasminogen activator

<220>
 <221> PEPTIDE
 <222> (381) ... (386)
 <223> Hexahistidin affinity tag

<400> 25

Met Ala Glu Ser His Leu Leu Gln Trp Leu Leu Leu Leu Leu Pro Thr
1 5 10 15

Leu Cys Gly Pro Gly Thr Ala Ala Trp Phe Pro Ile Pro Leu Pro Tyr
20 25 30

Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile Pro
35 40 45

Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val Pro
50 55 60

Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser Val
65 70 75 80

Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val Cys
85 90 95

Arg Leu Val Leu Arg Cys Ser Met Lys Pro Ser Ser Pro Pro Glu Glu
100 105 110

Leu Lys Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile
115 120 125

Ile Gly Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala
130 135 140

Ile Tyr Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly
145 150 155 160

Ser Leu Ile Ser Pro Cys Trp Val Ile Ser Ala Thr His Cys Phe Ile
165 170 175

Asp Tyr Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg
180 185 190

Leu Asn Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu
195 200 205

Ile Leu His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp
210 215 220

Ile Ala Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro
225 230 235 240

Ser Arg Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro
245 250 255

Gln Phe Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser
260 265 270

Thr Asp Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu
275 280 285

Ile Ser His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val
290 295 300

Thr Thr Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser
 305 310 315 320
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg
 325 330 335
 Met Thr Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys
 340 345 350
 Asp Lys Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile
 355 360 365
 Arg Ser His Thr Lys Glu Gln Asn Gly Leu Ala Leu His His His His
 370 375 380
 His His
 385

<210> 26
 <211> 383
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> SIGNAL
 <222> (1) ... (20)
 <223> Signal sequence of the urokinase plasminogen activator

<220>
 <221> PEPTIDE
 <222> (23) ... (298)
 <223> Low molecular weight two-chain urokinase-plasminogen activator

<220>
 <221> PEPTIDE
 <222> (299) ... (377)
 <223> Coding sequence of the mature surfactant protein B

<220>
 <221> PEPTIDE
 <222> (378) ... (383)
 <223> Hexahistidin affinity tag

<400> 26

Met Arg Ala Leu Leu Ala Arg Leu Leu Leu Cys Val Leu Val Val Ser
 1 5 10 15

Asp Ser Lys Gly Ser Asn Lys Pro Ser Ser Pro Pro Glu Glu Leu Lys
 20 25 30

Phe Gln Cys Gly Gln Lys Thr Leu Arg Pro Arg Phe Lys Ile Ile Gly
 35 40 45

Gly Glu Phe Thr Thr Ile Glu Asn Gln Pro Trp Phe Ala Ala Ile Tyr
 50 55 60

Arg Arg His Arg Gly Gly Ser Val Thr Tyr Val Cys Gly Gly Ser Leu

| 65 | 70 | 75 | 80 |
|---|---|-----|-----|
| Ile Ser Pro Cys Trp Val | Ile Ser Ala Thr His Cys Phe Ile Asp Tyr | | |
| 85 | 90 | | 95 |
| Pro Lys Lys Glu Asp Tyr Ile Val Tyr Leu Gly Arg Ser Arg Leu Asn | | | |
| 100 | 105 | | 110 |
| Ser Asn Thr Gln Gly Glu Met Lys Phe Glu Val Glu Asn Leu Ile Leu | | | |
| 115 | 120 | | 125 |
| His Lys Asp Tyr Ser Ala Asp Thr Leu Ala His His Asn Asp Ile Ala | | | |
| 130 | 135 | | 140 |
| Leu Leu Lys Ile Arg Ser Lys Glu Gly Arg Cys Ala Gln Pro Ser Arg | | | |
| 145 | 150 | 155 | 160 |
| Thr Ile Gln Thr Ile Cys Leu Pro Ser Met Tyr Asn Asp Pro Gln Phe | | | |
| 165 | 170 | | 175 |
| Gly Thr Ser Cys Glu Ile Thr Gly Phe Gly Lys Glu Asn Ser Thr Asp | | | |
| 180 | 185 | | 190 |
| Tyr Leu Tyr Pro Glu Gln Leu Lys Met Thr Val Val Lys Leu Ile Ser | | | |
| 195 | 200 | | 205 |
| His Arg Glu Cys Gln Gln Pro His Tyr Tyr Gly Ser Glu Val Thr Thr | | | |
| 210 | 215 | 220 | |
| Lys Met Leu Cys Ala Ala Asp Pro Gln Trp Lys Thr Asp Ser Cys Gln | | | |
| 225 | 230 | 235 | 240 |
| Gly Asp Ser Gly Gly Pro Leu Val Cys Ser Leu Gln Gly Arg Met Thr | | | |
| 245 | 250 | | 255 |
| Leu Thr Gly Ile Val Ser Trp Gly Arg Gly Cys Ala Leu Lys Asp Lys | | | |
| 260 | 265 | | 270 |
| Pro Gly Val Tyr Thr Arg Val Ser His Phe Leu Pro Trp Ile Arg Ser | | | |
| 275 | 280 | | 285 |
| His Thr Lys Glu Gln Asn Gly Leu Ala Leu Phe Pro Ile Pro Leu Pro | | | |
| 290 | 295 | 300 | |
| Tyr Cys Trp Leu Cys Arg Ala Leu Ile Lys Arg Ile Gln Ala Met Ile | | | |
| 305 | 310 | 315 | 320 |
| Pro Lys Gly Ala Leu Ala Val Ala Val Ala Gln Val Cys Arg Val Val | | | |
| 325 | 330 | | 335 |
| Pro Leu Val Ala Gly Gly Ile Cys Gln Cys Leu Ala Glu Arg Tyr Ser | | | |
| 340 | 345 | | 350 |
| Val Ile Leu Leu Asp Thr Leu Leu Gly Arg Met Leu Pro Gln Leu Val | | | |
| 355 | 360 | | 365 |
| Cys Arg Leu Val Leu Arg Cys Ser Met His His His His His His | | | |
| 370 | 375 | 380 | |

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